GenCore version 4.5 Copyright (c) 1993 - 2000 Com

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on:
                                                                                                                                                                                                                                                                                                                                                          score greater than and is derived by a
                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
    696
696
696
696
673
348.5
330.5
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323
319.5
                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                        d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-926-256-1
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Match
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2: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1981.DAT: *
2: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1981.DAT: *
3: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1982.DAT: *
4: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1983.DAT: *
4: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1983.DAT: *
5: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
5: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
7: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
8: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
9: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
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11: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1985.DAT: *
12: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1995.DAT: *
13: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1995.DAT: *
14: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1995.DAT: *
15: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1995.DAT: *
16: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1995.DAT: *
17: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1995.DAT: *
18: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1995.DAT: *
20: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1995.DAT: *
21: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1996.DAT: *
22: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1996.DAT: *
23: \SIDS1\gcgdata\hold-geneseq\geneseqp-embl\AA1996.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           October 3, 2002, 16:22:51;
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                                                                                                                                                                                                                                                      Length DB
    126
126
149
149
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130
131
132
133
133
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16
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    AAR71979
AAR7195627
AAR7196281
AAR385628
AAR38228
AAR38222
AAR38222
AAR38222
AAR38223
AAR38223
                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search time 29.94 Seconds (without alignments) 467.445 Million cell updates/sec
Snake venom derive Sequence of the pl Sequence of polype Sequence of polype Sequence of polype Botrocetin alpha s Sequence of polype Snake venom blood
                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                      Snake venom
Snake venom
                                                                                                                                                                     Snake venom
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derith
antith
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| | AAP94615 | 10 | 165 | ω · | 162 | 5 |
|--------------------|----------|------------|--------|----------|-------|-----------------|
| Vipera palestinae | AAR72234 | 16 | 43 | w | 162 | 44 |
| Human cancer assoc | AAB43568 | 21 | 183 | ω. | 166.5 | Ω |
| Human Pancreatitis | AAR57117 | <u>1</u> 5 | 175 | ω. | 166.5 | 2 |
| Mouse PAP. Mus mu | AAR54098 | 15 | 175 | ω | 166.5 | 11 |
| MUREG-2. Mus musc | AAR34536 | 14 | 173 | ω | 167 | 0 |
| | AAB18614 | 21 | 175 | 4 | 169.5 | 39 |
| Reg-2 protein. Ra | AAW95089 | 20 | 175 | 4. | 169.5 | 8 |
| Bovine pancreatic | AAR05904 | 11 | 175 | 4. | 169.5 | 37 |
| N-terminal sequenc | AAR23889 | 13 | 50 | 4. | 171 | 36 |
| Snake venom derive | AAY85632 | 21 | 44 | 4. | 172 | ω S |
| MUREG-1. Mus musc | AAR34535 | 14 | 165 | 4. | 174 | 34 |
| Mouse PAP. Mus mu | AAR54097 | 15 | 175 | 25.3 | 176.5 | ω |
| Human cancer assoc | AAB43737 | 21 | 174 | 5 | 181 | 32 |
| Human colon associ | AAB71666 | 22 | 166 | 5 | 181 | μ. |
| Human colon associ | AAB71653 | 22 | 166 | 5 | 181 | õ |
| Human reg protein. | AAR59288 | 15 | 166 | 5 | 181 | 29 |
| ш. | AAR06425 | 11 | 147 | 25.9 | 181 | 8 |
| Human reg protein | AAR66591 | 15 | 146 | 5 | 181 | 27 |
| | AAR66592 | 15 | 144 | 5 | 181 | 6 |
| | AAR66593 | 15 | 133 | 5 | 181 | 5 |
| ğ | AAP94614 | 10 | 165 | σ, | 185 | 24 |
| Sequence encoded b | AAP81514 | 9 | 166 | ς. | 187 | $\ddot{\omega}$ |
| Sequence of polype | AAR38224 | 14 | 125 | | 200.5 | 2 |
| Botrocetin beta su | AAR45157 | 14 | 125 | 9 | 203.5 | 21 |
| Ø | AAR23885 | 13 | 36 | 9 | 209 | õ |
| Sequence of polype | AAR38227 | 14 | 107 | 0 | 212 | 9 |
| ğ | AAR71978 | 16 | 3 8 | | 220 | 8 |
| Sequence of the pl | AAR24427 | 13 | 116 | 1 | 221 | 7 |
| Snake venom blood | AAM51544 | 22 | 146 | | 222.5 | 6 |
| lles | AAR72236 | 16 | 127 | ω. | w | 5 |
| 0 f | AAR38225 | 14 | 123 | <u>ი</u> | S | 4 |
| 0 | AAR38230 | 14 | 133 | 37.8 | | ω |
| Vipera palestinae | AAR72235 | 16 | 132 | 38.0 | 265.5 | 2 |

ALIGNMENTS

RESULT AAR71979

μ

AAR71979;

AAR71979 standard;

peptide;

126

₽

28-NOV-1995

(first entry)

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Disulfide-bond
Disulfide-bond
Disulfide-bond
           Fukuchi N,
Tanaka A,
                                                                                                                     Crotalus horridus horridus
WPI; 1995-139559/18
                                                                30-MAR-1995.
                                                                            W09508573-A.
                                         22-SEP-1993;
                                                    21-SEP-1994;
                            (AJIN ) AJINOMOTO KK
           Ishii K,
Yamamoto H,
                                                                                        Location/Qualifiers
4..15
32..120
95..112
                                        93JP-0236975
                                                    94WO-JP01555
            Kito M, Kobay
, Yoshimoto R;
                 Kobayashi
                  Η,
                  Nagano M;
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Antithrombotic peptide; snake venom; platelet binding inhibition; von Willebrand factors; Crotalus horridus horridus.

Snake venom derived antithrombotic peptide

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RESULT
AAY85627
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Best Local S
Matches 125
                                                                  Producing physiologically-active subunit peptides originating polymer proteins by denaturation and specific separation, with antigenicity but improved solubility and stability, e.g. blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR71978 and AAR71979 are snake venom derived antithrombotic peptides, prepared by cleaving the interpeptide but retaining the intrapeptide disulphide bonds of the original snake venom oligopeptide. These peptides have the advantage of avoiding significant thrombocytopenia when administered at the minimun dose, for in vivo inhibition of platelet von Willebrand factor
   peptide
              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single-chain antithrombotic peptide - obtained by cleaving an oligopeptide from snake venom to break inter-chain di:sulphide bonds but preserve intra-chain di:sulphide bonds
                                  Claim 15; Page 44; 51pp; Japanese.
                                                        platelet-binding inhibitors
                                                                                                                   WPI; 2000-664985/64.
                                                                                                                                                                                                          31-MAR-2000; 2000WO-JP02127
                                                                                                                                                                                                                                                                              Crotalus horridus
                                                                                                                                                                                                                                                                                                 Subunit peptide production; snake venom; rattlesnake; thrombolytic; von Willebrand's factor; blood platelet-inhibitory activity.
                                                                                                                                         Fukuchi N,
                                                                                                                                                               (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                     02-APR-1999;
                                                                                                                                                                                                                                  12-OCT-2000.
                                                                                                                                                                                                                                                         WO200059926-A1
                                                                                                                                                                                                                                                                                                                                      Snake venom
                                                                                                                                                                                                                                                                                                                                                            07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                       AAY85627 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Pages 44-45; 84pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                 AAY85627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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 invention relates to a method ide originating from a polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFTRPR 126
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125; Conservative
                                                                                                                                        Kageyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                      derived
                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                     99JP-0096073
                                                                                                                                                                                                                                                                               horridus
                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%;
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                                                                                                                                        Kito
                                                                                                                                                                                                                                                                                                                                                                                                        126
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Pred. No. 3.8e-74;
1; Mismatches 0;
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                                                                                                                                        Kayahara
 for the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           von Willebrand factor
 production of a with disulphide
                                                                                                                                         Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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subunit
bonds within
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Best Local S
Matches 125
                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
Disulfide-bond
                     Single-chain antithrombotic peptide - obtained by oligopeptide from snake venom to break inter-chain bonds but preserve intra-chain disulphide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and between subunits. The method comprises denaturing the protein or its subunit using a protein denaturing agent in a solution, removing the agent in the presence of a polyoxyalkyl polyether which reacts with a thiol group and unwinds the subunit, and separating the polyoxyalkyl polyether-bound subunit peptide. The method can be used for producing physiologically-active subunit peptides for polymer proteins e.g. snake venom-originated dimer peptide with blood platelet-inhibitory activity on von Willebrand's factor. The peptides produced have platelet-binding inhibitory, and thrombolytic activity. The present sequence represents a rattlesnake protein used in an example illustrating the method of the
                                                                        N-PSDB;
                                                                                                                      Fukuchi N,
                                                                                                                                               (AJIN ) AJINOMOTO KK
                                                                                                                                                                       22-SEP-1993;
                                                                                                                                                                                             21-SEP-1994;
                                                                                                                                                                                                                       30-MAR-1995
                                                                                                                                                                                                                                              W09508573-A.
                                                                                                                                                                                                                                                                                                                                Crotalus
                                                                                                                                                                                                                                                                                                                                                       Antithrombotic von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                          Snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR71981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR71981 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 kftrpr 126
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les 125; Conserv
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                                                                                    1995-139559/18.
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                                                                                                          Ą,
                                                                        AAQ89309
                                                                                                                                                                                                                                                                                                                                horridus horridus
                                                                                                            Yamamoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
                                                                                                                                                                                                                                                                                                                                                                                         antithrombotic oligopeptide
                                                                                                                      Ishii K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                      peptide; snake venom; platelet binding inhibition;
factors; Crotalus horridus horridus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                       93JP-0236975
                                                                                                                                                                                             94WO-JP01555.
                                                                                                                                                                                                                                                                    27..38
55..143
118..135
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.68;
                                                                                                                        Kito
                                                                                                          ito M, Kob
Yoshimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 696; DB 21;
Pred. No. 3.8e-74;
1; Mismatches 0;
                                                                                                                       Kobayashi
                                                                                                            77
                                                                                                                      Nagano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 126;
                                               cleaving
                                    di:sulphide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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Example 2;

Pages 47-48;

84pp; Japanese

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RESULT
AAY85628
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Best Local
This invention relates to a method for the production of a subunit peptide originating from a polymer protein with disulphide bonds within and between subunits. The method comprises denaturing the protein or its subunit using a protein denaturing agent in a solution, removing the agent in the presence of a polyoxyalkyl polyether which reacts with a thiol group and unwinds the subunit, and separating the polyoxyalkyl polyether-bound subunit peptide. The method can be used for producing physiologically-active subunit peptides for polymer proteins e.g. snake venom-originated dimer peptide with blood platelet-inhibitory activity
                                                                                                                                                                           Producing physiologically-active subunit peptides originating i polymer proteins by denaturation and specific separation, with antigenicity but improved solubility and stability, e.g. blood platelet-binding inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR/1978 and AAR/1979 are snake venom derived antithrombotic peptides, specifically from the snake venom oligopeptide AAR/1981, encoded by AAQ89309. These peptides have the advantage of avoiding significant thrombocytopenia when administered at the minimum dose, for in vivo
                                                                                                                                              Example 2; Page 47; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crotalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snake venom derived protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                             Fukuchi N,
                                                                                                                                                                                                                                                                                                                         (AJIN ) AJINOMOTO CO
                                                                                                                                                                                                                                                                                                                                                      02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000WO-JP02127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY85628 standard; protein; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 kftrpr 149
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Willebrand's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \tt dlecpsgwssydrycykpfkqemtwadaerfcseqakgghllsvetaleasfvdnvlyan
                                                                                                                                                                                                                                                                 2000-664985/64.
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                                                                                                                                                                                                                                                    AAC61144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        horridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of platelet von Willebrand factor binding.
                                                                                                                                                                                                                                                                                           Kageyama
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                                                                                                                                                                                                                                                                                                                                                      99JP-0096073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production; snake venom; rattlesnake; thrombolytic; factor; blood platelet-inhibitory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        horridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%;
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                                                                                                                                                                                                                                                                                           Kito
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Pred. No. 4.7e-74;
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                                                                                                                                                                                                                                                                                           Kayahara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                             Yamamoto
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RESULT AARZULT AARZULT
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Best Local S
Matches 125
                                        The PAA was purified from a solution of snake venom. Analysis of the peak inhibitory fractions by SDS-PAGE revealed 2 major proteins migrating with a mol. wt. 23-28 kD. Both were able to inhibit botrocetin and ristocetin induced platelet agglutination. They were called CHH-A and CHH-B. The earlier eluting subunit (CHH-B-beta) and later eluting subunit (CHH-B-alpha) were individually submitted to N-terminal sequence analysis. The complete amino acid sequence for the alpha and beta chains are given in AAR24426 and AAR24427.
                                                                                                                                                                                                                                                                                                                                                                                            Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit thrombus formation; for treatment of arteriosclerosis, atherosclerosis, acute myocardial infarction, chronic unstable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Platelet adherence inhibitor; platelet anti-adhesive; antithrombotic agent; von Willebrand Factor; platelet glycoprotein GPIb-IX complex.
                                                                                                                                                                                                                                                                                                             Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-199936/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crotalus horridus horridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of the platelet glycoprotein GPIb inhibitor alpha chain (CHH-B-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR24426 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORT-) COR THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-NOV-1990;
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les 125; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               von Willebrand's factor. The peptides produced have platelet-binding hibitory, and thrombolytic activity. The present sequence represents tilesnake protein used in an example illustrating the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFTRPR 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0614443
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                                                                                                                                                                                                                                                                                                          5pp;
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                                                                                                                                                                                                                                                                                                          English.
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Pred. No. 4.7e-74;
1; Mismatches 0,
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                                                    Query Match
Best Local
                                          Matches
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                                                                                                                           Alboaggregin B1 and B2 (collectively "AL-B"), may be obtained in substantially pure chemical form from venom. Each of AL-B1 and -B; comprise an about 23 kDa protein formed by an about 17 kDa polypeptide chain crosslinked to an about 14 kDa polypeptide chain by one or more interchain disulfide bonds. Each of the two polypeptide chains of AL-B1 and -B2 show strong homology to two of the chains of AL-A. AL-B1 and -B2 each comprise two non-identical
                                                                                                                                                                                                                                 New platelet-binding proteins obtained from snake venom -binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                                                                                                                           03-DEC-1991;
05-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Trimeresurus
                                                                                              Sequence
                                                                                                                  polypeptide chains.
                                                                                                                                                                                                               Claim 8; Page 48; 74pp; English.
                                                                                                                                                                                                                                                                              WPI; 1993-196991/24.
                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venom; snake; platelet-binding protein
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                                                     Local Similarity
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dcpsdwssfkqycyqivkelktwedaerfcseqandghlvsiesyreavfvaellsenvk 60
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                                                                                              130 AA;
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92US-0893929
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                                                    49.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.3%;
                                      Score 348.5; DB 14;
Pred. No. 3.8e-33;
"4-matches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 673; DB 13;
Pred. No. 2e-71;
1; Mismatches 3;
                                                              DB 14; Length 130;
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                                          13;
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                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL-A contains two types of polypeptide chains, with mol. wt. of about 18 kDa and about 15 kDa, respectively. Each of these two types of chains is actually composed of two subtypes. Thus, AL-A comprises four non-identical polypeptide chains. A possible variation of AAR38224 has been found, characterised by Asp at posn. three in lieu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New platelet-binding proteins obtained from snake venom -
binding of von Willebrand factor to platelet membrane
glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 45; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1991;
05-JUN-1992;
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                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQHSFICKFTR 124
                                                                                        sekhyvwiglrvqgkgqqcssewsdgssvhwdnlqekntrkcyglekraefrtwsnvycg 120
                                                                                                                                    YLTRYIWIGLRVQNKGQPC-----SSISYENLVD--PFECFMVSRDTRLREWFKVDCE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eqkhifmckf 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQQHSFICKF 122
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                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peng M;
                                                                                                                                                                                                                                                                                                                                                                                      131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide chain of alboaggregin A
                                                                                                                                                                                                                                                                       47.3%; llarity 45.8%; Conservative 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-0803630
92US-0893929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US10344.
131
                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                       Score 330.5; DB 1
Pred. No. 5.1e-31;
3; Mismatches 39
                                                                                                                                                                                                                                                                                                                 DB 14;
                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                     131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibit
                                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                         Gaps
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RESULT
AAR38226
ID AAR3
XX AAR3
AC Venc
XX A1b
CC Subb
CC Com
CC Subb
CC Com
CC
RESULT
AAR45156
ID AAR4
XX
AC AAR4
XX
DT 08-J
XX
DE Botr
                                                                                                                                                                                                                                                                                                                                     QY
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alboaggregin Bl and B2 (collectively "AL-B"), may be obtained in substantially pure chemical form from venom. Each of AL-B1 and -B2 comprise an about 23 kDa protein formed by an about 17 kDa polypeptide chain crosslinked to an about 14 kDa polypeptide chain by one or more interchain disulfide bonds. Each of the two polypeptide chains of AL-B1 and -B2 show strong homology to two of the chains of AL-A. AL-B1 and -B2 each comprise two non-identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New platelet-binding proteins obtained from snake venom - binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kirby EP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993
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  Botrocetin alpha subunit
                                                       08-JUN-1994
                                                                                                                                                          AAR45156 standard; protein; 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 47; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-196991/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1991;
05-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09311151-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trimeresurus albolabris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of polypeptide chain of alboaggregin Bl (AL-B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR38226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UTEM ) UNIV TEMPLE
                                                                                                                                                                                                                                                                                         121 gkhifmckf 129
                                                                                                                                                                                                                                                                                                                                              114 QQHSFICKF 122
                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                             tkynvwiglsvqnkeqqcssewsdgssvxyenlikpnpkkcfvlkkesefrtwsnvyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
                                                                                                                                                                                                                                                                                                                                                                                                                           dcpsdwssfkqycyqivkelktwedaexfcseqandghlvsiesyreavfvaellsenvk 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peng M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                    (first entry)
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92US-0893929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 330.5; DB Pred. No. 5.2e-313; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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RESULT 10
AAR38223
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                                                                                                                                                                                                                                                                                                                   Dр
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 62
                                                                                                                                           01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                             Botrocetin, isolated from Bothrops jararaca venom, is a disulfide-
linked heterodimer comprising an alpha subunit (AAR45156) and a beta
subunit (AAR45157). The protein is used to assay von Willebrand
factor in serum or plasma, for diagnosis of von Willebrand disease.
 03-DEC-1991;
                                                                                                                                                                                AAR38223 standard; protein; 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Willebrand's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of purified botrocetin and opt. ristocetin - for detection von Willebrand Factor in serum or plasma, for diagnosis of von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-407054/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP574621-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bothrops jararaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botrocetin; alpha subunit; von Willebrand factor; von
                    01-DEC-1992;
                                                           WO9311151-A.
                                                                              Trimeresurus
                                                                                                 Venom; snake; platelet-binding protein
                                                                                                                      Sequence of polypeptide chain of alboaggregin
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1993.
                                        10-JUN-1993
                                                                                                                                                                                                                                                       113
                                                                                                                                                                                                                                  121 aqknpfvcksppp 133
                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                 EQQHSFICKFTRP
                                                                                                                                                                                                                                                                         qssdlyawiglrvenkekqcssewsdgssvsyenvvertvkkcfalekdlgfvlwinlyc 120
                                                                                                                                                                                                                                                                                        EYLTRYIWIGLRYQNKGQPC------SSISYENLYDPF--ECFMVSRDTRLREWFKVDC
                                                                                                                                                                                                                                                                                                                                                          62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Y
                                                                                                                                                                                                                                                                                                                                                                                                           133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 8; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                               albolabris
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Titani K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUJITA HEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92EP-0305046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92EP-0305046
91US-0803630
                    92WO-US10344.
                                                                                                                                                                                                                                                      125
                                                                                                                                                                                                                                                                                                                                                                   46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snake venom; Bothrops jararaca;
Willebrand disease.
                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                         Score 323; DB
Pred. No. 4e-3
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    4e-30;
                                                                                                                                                                                                                                                                                                                                                                            DB 14;
                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                       A (AL-A)
                                                                                                                                                                                                                                                                                                                                                                             Length 133;
                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT
AAM5154
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New platelet-binding proteins obtained from snake venom binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL-A contains two types of polypeptide chains, with mol. wt. of about 18 kDa and about 15 kDa, respectively. Each of these two types of chains is actually composed of two subtypes. Thus, AL-A comprises four non-identical polypeptide chains. A possible variation of AAR38224 has been found, characterised by Asp at posn. three in lieu
                                                  Jang
                                                                                                                                                                                                                                                                                                         543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-196991/24.
  Halyxin as blood
                                                                       (BIOB-)
                                                                                            29-JUN-1999;
                                                                                                               29-JUN-2000; 2000KR-0036591
                                                                                                                                     15-JUN-2001
                                                                                                                                                        KR2001049671-A.
                                                                                                                                                                             Agkistrodon halys
                                                                                                                                                                                                          Snake; pit viper; venom;
                                                                                                                                                                                                                               Snake venom blood anticoagulant halyxin A chain.
                                                                                                                                                                                                                                                    10-JAN-2002
                                                                                                                                                                                                                                                                        AAM51543;
                                                                                                                                                                                                                                                                                            AAM51543 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UTEM ) UNIV TEMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1992;
                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                 112 CEOOHSFICKF 122
                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             | | : |:|||
ciqlnpfvckf 131
                               2001-637330/73
                                                                                                                                                                                                                                                                                                                                                                                    iqskehyvwiglkvqnkeqqcssewsdgssvtyenliklymrkcgaleqesgfrkwinlg 120
                                                                                                                                                                                                                                                                                                                                                                                                          KEYLTRYIWIGLRVQNKGQPC-----SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
                      AAI71876
                                                                       BIOBUD CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 46; 74pp; English.
                                                  Jung GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                  (first
                                                                                            99KR-0025105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-0893929
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anticoagulation
                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%;
42.7%;
                                                     K i m
                                                                                                                                                                                                                                                  entry)
                                                     DS,
                                                                                                                                                                                                          halyxin; anticoagulant; thrombogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                             152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 319.5; DB Pred. No. 1e-29;
                                                     800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
 protein separated
                                                     BH,
                                                     Son
                                                     Ϋ́D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 134;
   from
   snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               60
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RESULT 12
AAR72235
ID AAR722
XX AAR722
XX Vipera
XX Vipe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SXCCCCXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snak venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence is the A chain of halyxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1993;
14-JAN-1994;
10-JUN-1994;
                                                                                                                                                                                                                                                         Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vipera palestinae;
platelet binding; v
                                                    AAR72235 is a Vipera palestinae venom derived peptide. A peptide compsn. comprising AAR72235 and AAR7236 is claimed, it inhibits binding of platelets to von Willebrand factors and can therefore be used as an anti- thrombotic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vipera palestinae
                                                                                                                                                                                  Claim 5;
                                                                                                                                                                                                                                                                                                                                     WPI; 1995-147392/19.
                                                                                                                                                                                                                                                                                                                                                                                    Fukuchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLTRYIWIGLRVQNKGQPC------SSISYENLVDDPEE--CFMVSRDTRLREWFKVDCE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 palestinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
                                                                                                                                                                               Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Ishii K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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94JP-0002691.
94JP-0128518.
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                                                                                                                                                                             37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    venom derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21pp; Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          venom; antithrombotic
von Willebrand factor.
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                                                                                                                                                                                                                                                                                                                                                                                    Kaida K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 300.5; DB 22
Pred. No. 2.2c-27;
9; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                    Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                      Query Match
Best Local Similarity
Matches 51; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                              New platelet-binding proteins obtained from snake venom -binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                    Echicetin, is obtained in substantially pure chemical for from venom, as an about 26 kDa protein which likely comprises a dimer composed of two types of chains. One chain type has a mol. wt. of about 15 kDa and the other has a mol. wt. of about 13 kDa. The individual polypeptide chains are held together by one or more interchain disulfide bonds.
                                                                                                                                                                                                                                         Claim 10; Page 49; 74pp; English.
                                                                                                                                                                                                                                                                                                               WPI; 1993-196991/24.
                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-1991;
05-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of polypeptide chain of alboaggregin-like protein called echicetin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                            (UTEM ) UNIV TEMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Echis carinatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venom; snake; platelet-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR38230 standard;
                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYLTRYIWIGLRVQNKGQPCSS------ISYENLVDPFECFMYSRDTRLREWFKVDCE 113
                    DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
                                                                                                                                  133 AA;
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.0%;
llarity 39.1%;
Conservative 2
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92US-0893929.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                37.8%;
                                                                      32;
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                                                                                 Score 264.5; DB 1
Pred. No. 3.2e-23;
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                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
 ---SSISYENLVDPFECFMVSRDTRLREWFKVD 111
                                                                                           DB 14; Length 133;
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                                                                      Indels
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RESULT 1
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Best Local
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                                                                                                                                                                                                                                            AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL-A contains two types of polypeptide chains, with mol. wt. of about 18 kDa and about 15 kDa, respectively. Each of these two types of chains is actually composed of two subtypes. Thus, AL-A comprises four non-identical polypeptide chains. A possible variation of AAR38224 has been found, characterised by Asp at posn. three in lieu
                                                                                                                                                                                                                                                                                                                                                        New platelet-binding proteins obtained from snake venom binding of von Willebrand factor to platelet membrane glycoprotein IB, useful in therapy, diagnosis and surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1991;
05-JUN-1992;
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                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 47; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-196991/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kirby EP, Peng M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venom; snake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of polypeptide chain of alboaggregin A (AL-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UTEM ) UNIV TEMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
111 cssthsfvcef 121
                       112 CEQQHSFICKF 122
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                                                                                            ANKEYLTRYIWIGLRVQNKGQPCSS-----ISYENLVDPFECFMVSRDTRLREWFKVD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEQQHSFICKFTRPR 126
                                              an----lvwigl--snlwngcnsqwsdgtxldykxwreqfec-lvsrttn-newlsmd
                                                                                                                                               l Similarity
52; Conserv
                                                                                                                                                                                                           123 AA;
                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         platelet-binding
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92US-0893929
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                                                                                                                                                          36.6%;
39.7%;
                                                                                                                                               23;
                                                                                                                                             Score 255.5; DB 14; Length 123; Pred. No. 3.3e-22; 3; Mismatches 35; Indels 21;
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AAR72236

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Search completed: October Job time: 119 sec
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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1993;
14-JAN-1994;
10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                  Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic agent
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                      AAR72236 is a Vipera palestinae venom derived peptide. A peptide compsn. comprising AAR72235 and AAR72236 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an anti- thrombotic agent.
                                                                                                                                                                                                                                                                                                                           Claim 5; Pages 19-20; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-147392/19.
                                                                                                                                                                                                                                                                                                                                                                                                                   Fukuchi N, Ishii K, Kaida K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vipera palestinae; venom; antithrombotic agent; platelet binding; von Willebrand factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vipera palestinae venom derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vipera palestinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR72236 standard; peptide; 127 AA.
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115 ykficksrvpr 125
                                                                            116 HSFICKFTRPR 126
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                                                                                                127 AA;
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94JP-0002691.
94JP-0128518.
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Result
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Maximum
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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Maximum Match 100%
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1 DLECPSGWSSYDR
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Copyright (c) 1993 - 2000
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US-08-612-840A-8
US-07-614-443A-1
US-08-294-859-1
US-08-294-859-1
US-08-81-676-1
US-07-893-929A-1
PCT-US92-10344-7
PCT-US92-10344-7
PCT-US92-10344-2
US-07-893-929A-3
PCT-US92-10344-2
US-07-893-929A-4
US-07-893-929A-6
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; TOPOLOGY: 1: ; MOLECULE TYPE: US-08-612-840A-2

SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acid amino acid linear peptide

acids

| RESULT 1 US-08-612-8 Sequence Patent NA APPLIC CORRES ADDI STAN COURTS STAN COURTS STAN COURTS SOFT CURRES SOFT APPLIC COMME APPLIC COMPUT APPLIC APPLIC COMPUT APPLIC COMPUT APPLIC COMPUT APPLIC COMPUT APP | 4444 5000 54444 54400 54400 |
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| NG ANTI-THE ODUCING THE elland, Maj s Highway, s | US-07-614-443A-5 US-08-294-859-5 US-08-481-676-5 US-07-893-929-10 PCT-US92-10344-10 US-08-461-530A-4 US-08-822-261-3 US-08-822-261-3 US-08-822-261-3 US-08-822-261-3 US-08-822-263-3 US-08-822-103-44-8 US-08-822-103-44-8 US-08-729-103-44-8 US-08-822-261-4 |
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| | 4747378887344277555 |
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Query Match

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; MOLECULE TYPE: peptide US-08-612-840A-8
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US-08-612-840A-8
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                                                   Matches 125;
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Patent No. 585612
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/612,80
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                   FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5856126man F. Oblon
REGISTRATION NUMBER: 24,618
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CORRESPONDENCE ADDRESS:
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APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
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                   1 DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNYLYAN 60
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INFORMATION:
                                                                                                                                                                               : 149 amino acids
amino acid
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1755 S. Jefferson Davis Highway, Suite 400
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NAGANO, Mitsuyo
                                                     Conservative
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ISHII, Koichi
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                                               Score 696; DB 2; L
Pred. No. 9.7e-79;
Pred. No. 9.7e-79;
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RESULT 4
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US-07-614-443A-1
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Sequence 1, Application US/08294859 Patent No. 5679542
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
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NAME: MUTASHIGE, Kate H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ANTITHROMBOSIS AGENTS NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
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TELEFAX: 706141
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nes 122; Conserv
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                Conservative
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Road
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Pred. No. 5.6e-76;
1; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.

TITLE OF INVENTION: ANTITHROMBOSIS AGENTS NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTITHROMBOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                         121 KFTRPR 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-AUG-1994
CLASSIFICATION: 435
FTORMEY ACTION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                         COUNTRY:
                                                                                                                                                             STREET:
                                                                                                                                              CITY:
                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYLTRYIWIGLRVQNKGQPCSSIYSENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
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                                                                                                                                              Washington, D.C.
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                                                                                                                                                             E: Morrison & Foerster 2000 Pennsylvania Ave. N.W., Suite 5500
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                                                                                                                                                                                                                                      ANTITHROMBOSIS AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 673; DB 1; Length 127; Pred. No. 5.6e-76; 1; Mismatches 3; Indels
                    Version #1.25
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US-07-893-929A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MUTBSHLEY: 29,959
REGISTRATION NUMBER: 2803
REFERENCE/DOCKET NUMBER: 2803
TELECOMMUNICATION INFORMATION:
"MPT.EPHONE: (202) 887-1500
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,92
FILING DATE: 1992060
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: UFILING DATE: 07-JUN-1CLASSIFICATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
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                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KEYLTRYIWIGLRYONKGOPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                    STREET: 406 University: Philadelphia
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Temple University - Of The Common ADDRESSEE: wealth System of Higher Education STREET: 406 University Services Building
                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                        Diskette,
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                                                                                                                                    US/07/893,929A
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                                                                                                                                                                                                                            3.50 inch, 720
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Pred. No. 5.6e-76;
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REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:

30,480

6056-126 (CIP) 1

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US-07-893-929A-7
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Best Local Similarity
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                                                       TELEX: None INFORMATION FOR SEQ ID NO: 7:
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TELEX: NO. 5336667e
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                  CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 07/803,630
APPLICATION NUMBER: 3, 1991
                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                         NAME: MONACO, DANIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                                                  FILING DATE: December 3, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 19921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Philadelphia
STATE: Pennsylvania
                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 EYLTRYIWIGLRVQNKGQPC-----SSISYENLV--DPFECFMVSRDTRLREWFKVDC 112
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                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                         (215) 568-5549
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                                                                                                                                               6056-126 (CIP) 1
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TOPOLOGY: US-07-893-929A-1
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   Matches
               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                    TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO. 5336676
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 60 TELECOMMUNICATION INFORMATION: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS
SOSTWARE: WorldPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/
FILING DATE: 19920605
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
APPLICATION NUMBER: 07/803,630
APPLICATION DECEMBER 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MODACO, Daniel A.
REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Disketta
COMPUTER: IBM PS/2
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 EQKHIFMCKF 127
                                                                                                                      TYPE: !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 EQQHSFICKF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 406 University Services Building CITY: Philadelphia STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KY---HVWIGLSVQNKGQQCSSEWSDGSSVSYENLVKPNPKKCFVLKKESEFKTWSNVYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 EYLTRYIWIGLRVQNKGQPC------SSISYENLV--DPFECFMVSRDTRLREWFKVDC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                 H: 131 amino acids
AMINO ACID
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Peng, Man-l
 Conservative
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wealth System of Higher Education
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               48.4%; Score 338.5; DB 1
47.3%; Pred. No. 1.8e-34;
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Agonists Which Bind To Platelet
Membrane Glycoprotein Ib
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 Mismatches
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                                 DB 1;
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39;
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 Indels
                                 Length 131;
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9;
Gaps
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                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                   Query Match 48.4%;
Best Local Similarity 47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/803,63
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3383
TELEPHONE: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USS
FILING DATE: 19921201
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 07/803,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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121
                                  114 QQHSFICKFTR 124
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ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
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                                                                                                               63
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                                                                                                                                                      DCPSDWSSYDQYCYRVFKRLQTWEDAERFCSEQANDGHLVSIESAGEADFVTQLVSENIR 60
HEYPFVCKFXR 131
                                                                        SEKHYVWIGLRVQGKGQQCSSEWSDGSSVHYDNLQEKNTRKCYGLEKRAEFRTWSNVYCG 120
                                                                                                             YLTRYIWIGLRVQNKGQPC-----SSISYENLVD--PFECFMVSRDTRLREWFKVDCE 113
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AMINO ACID
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                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                 Score 338.5; DB 5;
Pred. No. 1.8e-34;
21; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6056-126 (CIP) 1
                                                                                                                                                                                                                                                                   Length 131;
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PCT-US92-10344-5
; Sequence 5, Application PC/TUS9210344
; GENERAL INFORMATION:
; APPLICANT: Kirby, Edward P.
; APPLICANT: Peng, Man-ling
; TITLE OF INVENTION: Alboaggregins
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US-07-893-929A-5
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                                                                                                                RESULT 11
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Matches
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APPLICANT: Kirby,
APPLICANT: Peng, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6556
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPHONE: (215) 568-5549
TELEPRAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: NO. 5336667e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/893,7
FILING DATE: 19920605
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
APPLICATION NUMBER: 07/803,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Peng, Man-ling TITLE OF INVENTION: Alboaggregins: Platelet TITLE OF INVENTION: Agonists Which Bind To Platelet TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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STATE: Pennsylvania
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                                                                                                                                                                                                                                                    61 TTKYNVWIGLSVQNKEQQCSSEWSDGSSVXYENLIKPNPKKCFVLKKESEFRTWSNVYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                            QKHIFMCKF 129
                                                                                                                                                                                                                QQHSFICKF 122
                                                                                                                                                                                                                                                                                          YLTRYIWIGLRVQNKGQPC-----SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 132 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                         47.7%; Score 333.5; DB 1;
47.3%; Pred. No. 7.6e-34;
tive 24; Mismatches 35;
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Alboaggregins:

Platelet

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RESULT 12
US-07-893-929A-2
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                                                                                                                                                                                                                Sequence 2, Application Patent No. 5336667 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9
FILING DATE: 19921201
                                                                                                              TITLE OF INVENTION: Alboaggregins: Platelet TITLE OF INVENTION: Agonists Which Bind To Platelet TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: AMINO ACID
                                                                            NUMBER OF SEQUENCES: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MONACO, DAniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                          APPLICANT: Kirby, Edward P. APPLICANT: Peng, Man-ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/80
FILING DATE: December 3,
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ADDRESSEE: Temple University - Of The Common-ADDRESSEE: wealth System of Higher Education STREET: 406 University Services Building CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                             61 TTKYNVWIGLSVQNKEQQCSSEWSDGSSVXYENLIKPNPKKCFVLKKESEFRTWSNVYCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
2IP: 19122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DCPSDWSSFKQYCYQIVKELKTWEDAEKFCSEQANDGHLVSIESYREAVFVAELLSENVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                        Application US/07893929A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.7%; Score 333.5; DB 5 nilarity 47.3%; Pred. No. 7.6e-34; Conservative 24; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (215) 568-5549
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er 3, 1991
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RESULT 13
PCT-US92-10344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9210344 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803
FILING DATE: December 3, 1
ATTORNEY/AGENT INFORMATION:
NAME: MONACO, DANIEL A.
REGISTRATION NUMBER: 30,48
                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CIQLNPFVCKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 CEQQHSFICKF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 15...

OPERATING SYSTEM: MS-LL

OPER
APPLICATION NUMBER: F
FILING DATE: 19921201
                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 406 University Services Building CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Temple University - Of The Common ADDRESSEE: wealth System of Higher Education
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IQSKEHYVWIGLKVQNKEQQCSSEWSDGSSVTYENLIKLYMRKCGALEQESGFRKWINLG 120
                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KEYLTRYIWIGLRVQNKGQPC-----SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DFHCLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETMGEADFVAQLISEN 60
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                                                                                                                                                                                                                                                                                            19122
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                                                                                                                                                                                                                                                                                                                                                                Pennsylvania
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(215) 568-5549
                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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                                                                                                                                                                                                                 Diskette, 3.50 inch, 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19920605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.7%;
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er 3, 1991
                                 PCT/US92/10344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/07/893,929A
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Pred. No. 4.2e-32;
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CLASSIFICATION:

07/803,630

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Kirby, Edward P.

APPLICANT: Peng, Man-ling

TITLE OF INVENTION: Alboaggregins: Platelet

TITLE OF INVENTION: Agonists Which Bind To Platelet

TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NUMBER: US/07/8
FILING DATE: 19920605
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SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3883
TELEPHAX: (215) 568-5549
                                                                       FILING DATE: 19920605
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: December 3, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
REFERENCE/DOCKET NUMBER: 60
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ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 19122
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                                  NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Monaco, Daniel A REGISTRATION NUMBER: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYLTRYIWIGLRVQNKGQPC-----SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFHCLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETMGEADFVAQLISEN 60
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                   6056-126 (CIP) 1
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PCT-US92-10344-9
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GENERAL INFORMATION:
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                                                                                                                                                  CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION UMBER: 07/803,630

PILLING DATE: December 3, 1991

ATTORNEY/AGENT INFORMATION:

NAME: MONACO, DANIEL A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-12

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383
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INFORMATION FOR SEQ ID NO:
                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: 19921201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
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                                                                          SEQUENCE CHARACTERISTICS:
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ZIP: 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS,
OPERATING SYSTEM:
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ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 37.8%; Score 264.5; DB 1
Local Similarity 37.8%; Pred. No. 2.8e-25;
nes 51; Conservative 32; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 133 amino acids TYPE: AMINO ACID
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                                                     LENGTH:
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                                   1: 133 amino acids
AMINO ACID
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(215) 56
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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| S52781 S28764 | T29536 | 150421 | A38609 | S49126 | S48719 | T46256 | T42630 | A39808 | A53210 | S57653 | в56829 | A54423 | A55182 | A28452 |
| neurocan - mouse | hypothetical prote | aggrecan precurson | lectin, galactose | brevican precurso | phospholipase-A(2) | brevican - human | aggrecan - bovine | proteoglycan core | phospholipase A2 | brevican precurso | alboaggregin-B alı | brevican precurso | aggrecan precurso | proteoglycan core |

ALIGNMENTS

coagulation factor IX-binding protein A chain - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 13-Mar-1998

C; Accession: JC4329

RESULT JC4329

| RESULT 2 A47267 A47267 A47267 A47267 A57267 A67267 | Qy 63 YLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCE 113 | Query Match Query Match Query Match Query Match 49.3%; Score 344.5; DB 2; Length 129; Best Local Similarity 48.4%; Pred. No. 1.7e-28; Matches 62; Conservative 24; Mismatches 33; Indels 9; Gaps 2; Qy 3 ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62 1 : | C;Accession: JC4329 R;Atoda, H.; Tshikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T. J. Blochem. 118, 965-973, 1995 A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus f A;Reference number: JC4329; MUID:96318509 A;Accession: JC4329 A;Molecule type: protein A;Residues: 1-129 < ATO> C;Comment: This protein binds calcium. C;Superfamily: tetranectin; C-type lectin homology C;Keywords: anticoagulant; blood coagulation; calcium binding; venom F;2-127/Domain: C-type lectin homology < LCH> F;2-1330-127,102-119/Disulfide bonds: #status predicted |
|---|---|---|--|

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A; Molecule type: protein
A; Residues: 24-152 <ARTO>
A; Residues: 24-152 <ARTO>
C; Superfamily: tetranectin; C-type lectin homology
C; Superfamily: tetranectin; C-type lectin on; glycoprotein; hemolymph; lectin
F; 1-23/Domain: signal sequence #status predicted <STG>
F; 24-152/Product: factor IX/X binding protein chain A #status predicted <MAT>
F; 25-150/Domain: C-type lectin homology <LCH>
F; 25-36,53-150,125-142/Disulfide bonds: #status predicted
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R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; S
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally
A;Reference number: A37958; MUID:91129280
A;Accession: B37958
A;Molecule type: protein
A;Residues: 1-40 < MUID:
C;Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemagglutinin; heterodimer; venom
F;2-128/Domain: C-type lectin homology CCCHP
F;2-13,30-128/L03-120/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: venom R;Atoda, H.; Hyuga, M.; Morita, T. J. Biol. Chem. 266, 14903-14911, 1991
A;Title: The primary structure of coagulation otein, tetranectin, and lymphocyte Fc epsilon A;Reference number: A39332; MUID:91332000
A;Accession: A39332
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R;MatSuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Biochem. Blophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from A;Reference number: JC4690; MUID:96184662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation factor IX/factor X-binding protein chain A precursor - habu C:Species: Trimeresurus flavoviridis (habu) C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
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A; Residues: 1-152 <MAT1>
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                     ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYLTRYIWIGLRVQNKGQPC-----SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                         45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.68;
                                                                                    Score 314.5; DB 2;
Pred. No. 2.6e-25;
6; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 323; DB 2; ]
Pred. No. 2.9e-26;
5; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                           factor IX/factor X-binding protein isolate
receptor for immunoglobulin E.
                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 133;
                                                                                                                              Length
                                                                                                                              152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g1402640
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                                                                                      9;
                                                                                  Gaps
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R;Chung, C.H.; Au, L.C.; Huang, T.F.
Blochem. Blophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of
A;Reference number: PC7027; MUID:99443731
A;Accession: PC7027
A;Molecule type: mRNA
A;Residues: 1-144 <CHU>
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-152 < CHE>
A; Cross-references: GB:AF176420
A; Experimental source: venom gland
A; Accession: PC7037
A; Molecule type: protein
A; Residues: 24-53;84-86;87-94;125-136;137-152 < CH2>
C; Superfamily: tetranectin; C-type lectin homology
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F; 24-152/Product: agkisacutacin alpha chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agkisacutacin alpha chain precursor - sharp-nosed v N.Alternate names: fibrinogenlytic venom protein C:Species: Agkistrodon acutus (sharp-nosed viper) C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 ().Accession: JC7134, PC7037 R;Cheng, X: Qian, Y: Liu, Q: Li, B.X.Y: Zhang, I Biochem. Biophys. Res. Commun. 265, 530-535, 1999 A;Title: Purification, characterization, and CDNA c A;Reference number: JC7134; MUID:20025379 A;Accession: JC7134
                                                                                                                                                                                                                                                                                                                                                                                 aggretin alpha chain - Malayan pit viper (fragment)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: PC7027
Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQDPFVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLTRYIWIGLRVQNKGQPC-----SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCSSGWSSYEGHCYKVFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLDFYIWIGLRVQGKVKQCNSEWSDGSSVSYENWIEAESKTCLGLEKETDFRKWVNIYCG
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57; Conserv
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                               42.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.48;
                               Score 296; DB 2
Pred. No. 2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 303.5; DB 2;
Pred. No. 3.5e-24;
4; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                                                                                                                                lectin homology
et aggregation; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.X.Y.; Zhang, M.; Liu, 530-535, 1999
Lion, and cDNA cloning o
             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sharp-nosed viper
                                                         DB 2;
             38;
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                                                       Length 144;
             Indels
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             12;
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             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
             4.
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Ditiscetin alpha chain - puff adder
N;Alternate names: von Wilebrand factor modulator protein
C;Species: Bitis arietans (puff adder)
C;Date: 31-Jan-1997 *sequence_revision 31-Jan-1997 *text_change 12-Feb-1999
C;Accession: JC5058; JC5916
R;Matsui, T; Hamako, J; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimur;
submitted to JIPID, January 1997
A;Description: Complete amino acid sequence of bitiscetin, a novel von willebrail A;Reference number: JC5058
A;Contents: snake venom
A;Accession: JC5058
A;Ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 24-50;59-83;102-107;112-114 <CH2>
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkisacutacin beta chain #status exp
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 FVCKF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKTDLVWIGLKNIWNGCYWKWSDGTKLDYKDWREQFEC-LVSR-TVNNEWLSMDCGTTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCPSEWSSYEGHCYKPFDEPKTWADAEKFCTQQHKGSHLASFHSSEEADFV--VTLTTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE
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Pred. No. 9.7e-20;
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                                                            K.; Fujimura,
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                                                            02
          coagulation factor X activating enzyme (EC 3.4.24.-) light chain - C;Species: Vipera russelli (Russell's Viper) C;Date: 04-Max-1993 #sequence_revision 18-Nov-1994 #text_change 28-C;Accession: B42972 R;Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Mor J. Biol. Chem. 267, 14109-14117, 1992 A;Title: Coagulation factor X activating enzyme from Russell's vipe
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B42972
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Russell's viper venom (RVV-X).

Morita, T.; Iwanaga,

Russell's

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A; Experimental source: venom C; Comment: This protein is a modulator of a von Willebrand C; Superfamily: tetranectin; C-type lectin homology C; Keywords: venom F; 4-125/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-146 <CHU>
A; Residues: 1-146 <CHU>
A; Experimental source: venom gland
C; Superfamily: tettanectin; C-type lectin homology
C; Keywords: disulfide bond; platelet aggregation;
                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 263, 723-727, 1999 A; Title: Molecular cloning and sequence analysis (A; Reference number: PC7027; MUID:99443731 A; Accession: JC7105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggretin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete amino acid
A;Reference number: JC5916
A;Accession: JC5916
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Best Local Similarity
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                                                                                                                                                                                                                                             Query Match
Best Local
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138
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                                                                                                                                                                                                                           Local Similarity hes 49; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPGCLPDWSSYKGHCYKVFKKVGTWEDAEKFCVENS--GHLASIDSKEEADFVTKLA---
                                                                                                                                                                   ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFYDNVLYANKE 62
                                                                      LKANLVWMGL--SNIWHGCNWQWSDGARLNYKDWQEQSEC-LAFRGVH-TEWLNMDCSST 137
CSFVCKF
                                  HSFICKE
                                                                                                            YLTRYIWIGLRVQNKGQPC----
                                                                                                                                                 DCPSGWSSYEGHCYKPFNEPKNWADAERFCKLQPKHSHLVSFQSAEEADFV--VKLTRPR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQTLTKFVYDAWIGLRDESKTQQCSPQWTDGSSVVYENVDEPTKCFGLDVHTEYRTWTDL
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144
                                  122
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                                                                                                                                                                                                                           19;
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                                                                                                                                                                                                                                             Score 237.5; DB :
Pred. No. 2.4e-17,
                                                                                                            --SSISYENLYDPFECFMVSRDTRLREWFKVDCEQQ 115
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115 RKKSFVCKY 123

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C:Superfamily: tetranectin; C-type lectin no
C:Keywords: venom
F;4-121/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-125 <MA2>
A; Residues: 1-125 <MA2>
A; Experimental source: venom
C; Comment: This protein is a modulator of a von Willebrand factor modulator.
C; Superfamily: tetranectin; C-type lectin homology
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A;Note: sequence extracted from NCBI backbone (NCBIP:108408)
A;Note: sequence extracted from NCBI backbone (NCBIP:108408)
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hydrolase; metalloproteinase; venom; zinc
F;4-121/Domain: C-type lectin homology <LCH>
F;4-15,32-121,98-113/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; O
Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A;Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: JC5059; JC5917
R;Matsul, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; submitted to JIPID, January 1997
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bitiscetin beta chain - puff adder
bitiscetin beta chain - puff adder
C;Species: Bitis arietans (puff adder)
C;Species: Bitis arietans (puff adder)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 12-Feb-1999
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A;Contents: V. r. siamensis
A;Accession: B42972
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                                                                                                                                                                                                                                                                                                                                                                                                                          ;Superfamily: tel;Keywords: venom
                                                                                                                                                                                                                                                                                                                           Query Match
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                       QQHSFICKF 122
                                                                                                                                                                                                  DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
                                                                                                                                                                           DEGCLPDWSSYKGHCYKVFKVEKTWADAEKFCKELVNGGHLMSVNSREEGEFISKL--AL 58
                                                                         EKMRIVLVWIGL--SHFWRICPLRWTDGARLDYRALSDEPICFVA--ESFHNKWIQWTCN 114
                                                                                                                         KEYLTRYIWIGLRVQNKGQPC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
47; Conser
                                                                                                                                                                                                                                                                            45; Conser
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.0%;
36.7%;
                                                                                                                                                                                                                                                                       29.8%; Score 208.5;
34.9%; Pred. No. 2e-
live 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 230.5; DB 2;
pred. No. 1e-16;
2; Mismatches 46;
                                                                                                                           -SSISYENLVDPFECFMVSRDTRLREWFKVDCE 113
                                                                                                                                                                                                                                                                                                 2e-14;
                                                                                                                                                                                                                                                                            48;
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                                                                                                                                                                                                                                                                                                                         Length 125;
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                                                                            bottocetin beta chain - jararaca
N.Alternate names: two chain botrocetin beta chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: B47267; C37958
R;Usami, Y;; Fujimura, Y; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulate
A;Reference number: A47267; MUID:93157385
                                                                                                                                                                                                                                                                                                                         RESULT
B47267
                     A; Molecule type: protein A; Residues: 1-125 <USA>
                                                                         A; Reference number: A; Accession: B47267
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A; Experimental source: venom
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factor modulator

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A;Experimental source: venom
R;Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A;Title: The primary structure of coagulation factor IX/factor X-binding protein cotein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000
A;Accession: B39332
A;Reference number: A39332; MUID:91332000
A;Accession: B39332
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: tetranectin; C-type lectin homology C;Keywords: anticoagulant; blood coagulation; lectin; venom F;1-23/Domain: signal sequence *status predicted <SIG>F;24-146/Product: factor IX/X binding protein chain B *status F;25-142/Domain: C-type lectin homology <LCH>F;25-36,53-142,119-134/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Blood coagulation factor IX-binding protein from the venom A;Reference number: JC4329; MUID:96318509
A;Accession: JC4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation factor IX/factor X-binding protein chain A precursor - habu C;Species: Trimeresurus flavoviridis (habu) C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000 C;Accession: JC4691; B39332; JC4330 IS;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T. Biochem. Biophys. Res. Commun. 220, 382-387, 1996 A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein A;Reference number: JC4690; MUID:96184662 A;Accession: JC4691 MUID:96184662 A;Molecule type: mRNA B;Molecule type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, J. Biochem. 118, 965-973, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 24-146 < AT2>
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Best Local S
82
                                                                                                      63 YLTRYIWIGLRVQNKGQPC-----SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
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                                                                                                                                                                                                                                                                                                             ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
FGHSIFWMGL--SNVWNQCNWQWSNAAMLRYKAWAE--ESYCVYFKSTNNKWRSRACRMM 137
                                                                                                                                                                                                                                      DCPSDWSSYEGHCYKPFSEPKNWADAENFCTQQHAGGHLVSFQSSEEADFV--VKLAFQT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-146 <MAT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 33.9
43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 204.5; DB 2;
Pred. No. 6.2e-14;
3; Mismatches 48;
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A; Accession: C37958
A; Accession: C37958
A; Molecule type: protein
A; Residues: 1-40 <FUJ>
C; Complex: heterodimer of alpha (see PIR:A47267) and beta (C; Superfamily: tetranectin; C-type lectin homology C; Keywords: hemaggluthin; heterodimer; venom
F; 2-121/Domain: C-type lectin homology <ICH>
F; 2-13, 30-121, 98-113/Disulfide bonds: #status experimental
F; 75/Disulfide bonds: interchain (to alpha-80) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: This protein inhibits agglutination of fixed llebrand factor and alboaggregins. C;Superfamily: tetranectin; C-type lectin homology C;Keywords: anticoagulant; dimer F;2-119/Domain: C-type lectin homology <LCH> F;2-13,30-119,96-111/Disulfide bonds: #status predicted
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R;Peng, M.; Holt, J.C.; Niewiarowski, S.
Biochem. Biophys. Res. Commun. 205, 68-72, 1994
A;Title: Isolation, characterization and amino acid sequence
A;Reference number: JC2415; MUID:95091801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              echicetin beta chain - saw-scaled viper
C;Species: Echis carinatus (saw-scaled viper)
C;Date: 21-Mar-1995 #sequence_revision 26-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: sequence extracted from NCBI backbone (NCBIP:124086)
R; Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui,
Biochemistry 30, 1957-1964, 1991
                                                                       B
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RESULT
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Best Local
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                                                                                                                    117
                                                                                                                                                                  61 -MELVWIGL-
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                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 39; Conserv
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                                                                       YFVCK 120
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                                                                                                                    SFICK 121
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                                                                                                                                                                                                             LTRYIWIGLRVQNKGQPC-----SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
                                                                                                                                                                                                                                                                CLPDWSVYEGYCYKVFKERMNWADAEKFCMKQVKDGHLVSFRNSKEVDFMISLAFPMLK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFQSKEEADFVRSL---TSE 57
                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  27.4%; Score 191.5; DB 2 31.2%; Pred. No. 1.2e-12;
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Pred. No. 6.7e-14;
6; Mismatches 39;
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                                        C; Genetics:
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A;Molecule type: protein
A;Residues: 23-47 <DEC>
R;Roulmi, P.; de Caro, J.; Bonicel, J.; Rovery, M.; de Caro,
R;BS Lett. 229, 171-174, 1988
A;Title: The disulfide bridges of the immunoreactive forms of
A;Reference number: S02419; MUID:88152214
A;Accession: S02419
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A;Title: Partial amino acid sequence of human A;Reference number: A25246; MUID:87099950
A;Accession: A25246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Rouimi, P.; Bonicel, J.; Rovery, M.; de Caro, A.
FEBS Lett. 216, 195-199, 197
A;Title: Cleavage of the Arg-Ile bond in the native polypeptide chain of human
A;Reference number: S01471; MUID:87219142
A;Accession: S01471
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A;Title: N-terminal sequence extension in
A;Reference number: S02767; MUID:89150292
A;Accession: S02767
A;Molecule type: protein
A;Residues: 34-73,'X',75-87,'R',89-98 <MON>
C;Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like
C;Comment: Intact regenerating islet lectin 1-alpha, lithostathine, inhibits the gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;de Caro, A.M.; Bonicel, J.J.; Rouimi, P.; de Caro, Eur. J. Biochem. 168, 201-207, 1987
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                                                                                                                                                                                                                                                                                                                                    R; Montalto, G.; Bonicel, J.;
Biochem. J. 238, 227-232, 19
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 33-48 < RO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 34-166 <DE1>
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A; Residues: 63-72;125-139;150-157;160-166 <ROU>
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A; Residues: 1-166 < TER>
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A;Title: A novel gene activated in regenerating islets
A;Reference number: A92704; MUID:88115343
A;Accession: B28351
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A; Residues: 1-166 <WAT>
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A;Accession: A35197
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GDB:132455;

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A:Map position: 2p12-2p12
A:Introns: 22/1; 61/3; 107/3; 145/1
A:Introns: 22/1; 61/3; 107/3; 145/1
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: glycoprotein; lectin; pancreas; pyroglutamic acid
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-166/Product: regenerating islet lectin 1-alpha #status experimental <MATP>
F:34-166/Product: pancreatic stone protein #status experimental <MATP>
F:36-162/Domain: C-type lectin homology <LCH>
F:33-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:33-34/Cleavage site: Arg-Ile (Trypsin) #status experimental
F:36-47,64-162,137-154/Disulfide bonds: #status experimental
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C;Species: Homo saptens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 28-May-1999
C;Accession: A45751
R;Giorgi, D.; Bernard, J.P.; Rouquier, S.; Iovanna, J.; Sarles, H.; Dagorn, J.C.
J. Clin. Invest. 84, 100-106, 1989
A;Title: Secretory pancreatic stone protein messenger RNA. Nucleotide sequence and expre A;Reference number: A45751; MUID:89292148
A;Accession: A45751
Search completed: October Job time: 116 sec
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Best Local Similarity 32.6
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                                                                                                                                                                                                                                                           ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 149
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| LT 2 LTRIAB ABAL_TRIAB STANDARD; PRT; 131 AA. P81111; 15-JUL-1998 (Rel. 36, Created) | 114 QQHSEICKFTRPR 126 ::: : 121 EKNVFNCKFQLPR 133 | 63 YLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCE 113 ::: | 3 ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62 : : : | Query Match 50.0%; Score 349.5; DB 1; Length 133; Best Local Similarity 48.1%; Pred. No. 4.6e-30; Matches 64; Conservative 24; Mismatches 36; Indels 9; Gaps | ID 2 13 BY SIMILARITY. ID 30 127 BY SIMILARITY. ID 102 119 BY SIMILARITY. CE 133 AA; 15962 MW; 386EAC519DFC674D C | | SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN. p; p23806; 11xx. expro; 1PR001304; lectin_c. m; pF00059; lectin_c; 1. | [1] SEQUENCE. SEQUENCE. TISSUE-Venom; Wang R., Kini M., Chung M.C.M.; Submitted (JUN-1998) to the SWISS-PROT data banki- SUBUNIT: HETEROTRIMER OF TWO ALPHA SUBUNITS AND ONE BETA SUBUNIT. | alpha subunit. rhodostoma (Ma. rhodostoma (Ma. Metazoa; Chorda a; Squamata; Sc. Crotalinae; Cal 8717; | I | A AGKRH |

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                                                                                             P22029;
01-AUG-1991 (Rel. 19, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
80trocetin, alpha chain (Platelet coagglutinin).
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80throps jararaca (Jararaca).
80throps jararaca (Jararaca).
80throps jararaca; Chordata; Craniata; Vertebrata;
10pidosauria; Squamata; Scleroglossa; Serpentes; Col
Viperidae; Crotalinae; Bothrops.
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SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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Trimeresurus albolabris (White-lipped pit viper).
Trimeresurus albolabris (White-lipped pit viper).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleost
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
             Titani K.;
                       MEDLINE=93157385; PubMed=8430107; Usami Y., Fujimura Y., Suzuki M.,
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                                                                SEQUENCE, AND DISULFIDE BONDS
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"Primary
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131 AA;
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two-chain botrocetin,
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Pred. No. 6.5e-29;
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P81115;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
Alboaggregin B alpha subunit.
Trimeresurus albolabris (White-lipped pit viper).
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Biochemistry 30:1957-1964(1991).

-I- FUNCTION: TWO-CHAIN BOTROCETIN FORMS AN ACTIVATED COMPLEX WITH VMF, AND THE COMPLEX THEN BINDS TO PLATELET GPIB, RESULTING IN
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata;
Lepidosauria; Squamata; Scleroglossa; S
Viperidae; Crotalinae; Trimeresurus.
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SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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MEDLINE=98189535; PubMed=9531050;
Kowalska M.A., Tan L., Holt J.C.,
                                             TISSUE-Venom;
                                                                   SEQUENCE
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FUNCTION: THERE ARE TWO DISTINCT FORMS OF FACTOR-DEPENDENT PLATELET COAGGLUTININ. THE FACTOR-DEPENDENT PLATELET THAN THE ONE-CHAIN BOOK ACTIVE THE BOOK ACTI
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E4CF4502946AC74B CRC64;
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Peng
                                                                                                                                                                                                                                                                                                                                                 132
                                                                                                                                                              Serpentes;
.
X
                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
.9e-27;
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Karczewski
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                                                                                                                                                              Colubroidea;
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Niewiarowski S.;

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RESULT 5
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Best Local :
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SEQUENCE
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InterPro; IPR001304; lectin_c.
                                                                                                 MEDLINE=98189535; PubMed=9531050; Kowalska M.A., Tan L., Holt J.C., Calvete J.J., Niewiarowski S.; "Alboaggregins A and B. Structure platelets.";
                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Alboaggregins A platelets.";
       Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                            SEQUENCE
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                                            DISULFIDE-LINKED.
                                                                                 Thromb. Haemost. 79:609-613(1998)
                                                                                                                                                                             NCBI_TaxID=8765;
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PROSITE;
                            InterPro;
                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGLUTINATION.
                                                               SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1,
                                                                       AGGLUTINATION
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                                                                                                                                                                                                                                                                                                                                                                       YLTRYIWIGLRVQNKGQPC------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                                                                                                                                                                                                                                                                                                                         QKHIFMCKF 129
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                                                                                                                                                                                                                                                                                                                                         QQHSFICKF 122
                                                                                                                                                                                                                                                                                                                                                                                                 DCPSDWSSFKQYCYQIVKELKTWEDAEXFCSEQANDGHLVSIESYREAVFVAELLSENVX
                                  P23806; 1IXX.
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PS00615;
                           IPR001304; lectin_c
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132 /
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C_TYPE_LECTIN_2;
C_TYPE_LECTIN_1; 1.
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(BY SIMILARITY).
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Pred.
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No. 3.2e-27;
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                                             THE
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                                                                                                            interaction with human
                                             C-TYPE
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                                                                                                                                Karczewski J.,
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                                                           2,
                                              LECTIN FAMILY
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RESULT 6
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Best Local S
Matches 56
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Best Local
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p81398;
p81398;
p81398;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Rhodocetin beta subunit.
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
viperidae; Crotalinae; Calloselasma.
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DISULFID
SEQUENCE
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DISULFID
SEQUENCE
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Submitted (JUN-1998) to the SWISS-PROT data
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                                                                                                                                                                                                                                                                             HSSP; P23806; 1IXX
                                                                                                                                                                                                                                                                                       -!- FUNCTION: INHIBITS PLATELET AGGLUTINATION.
-!- SUBUNIT: HETEROTRIMER OF TWO ALPHA SUBUNITS AND ONE BETA SUBUNIT
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                    TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHCB_AGKRH
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                 PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                            SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG
                                                                                                                                                                                                      Venom;
                                                                                                                                                                                                                                                                InterPro; IPR001304; lectin_c.
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 61
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                                                            DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
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                                               DFRCPTTWSASKLYCYKPFKEKKTWIEAERFCAKQAENGHLVSIGSAAEADFLDLVIVVN
 FDKQRYRAWTGLTERNLKWTNGASVSYENLYEPYIRKCFVVQPWEGKSKWYKADCEEKNA
                       KEYLTRYIWIGLRVQN-KGQPCSSISYENLVDPF--ECFMVSRDTRLREWFKVDCEQQHS 117
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56; Conserv
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129 i
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134
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15 B
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115 190 MW;
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42.78;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SF9D71FC86DE2435 CF
                                                                                           Score 316.5; DB 1
Pred. No. 1.3e-26;
0; Mismatches 39
                                                                                                                                                       C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
; EF4B318FAAC807AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129
                                                                                             39;
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RESULT 7
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PDB; 1IXX; 06 MAY-98.
InterPro; IPRO01304; lectin_c:
Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS000615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

Lectin; Calcium; Signal; 3D-structure.
DOMAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                     OF C-type lectin domains.";

Nat. Struct. Biol. 4:438-441(1997).

1- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.

1- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BON CONTROL OF THE C-TYPE LECTIN FAMILY.
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P23806; Q91246;
01-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
Coagulation factor IX/factor X-binding prot
                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsuzaki R., Yoshihara E., Yamada M., Shi "cDNA cloning of IX/X-BP, a heterogeneous protein from snake venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IX/X-BF).
Trimeresurus flavoviridis (Habu).
Tulmeresurus flavoviridis (Habu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                             CHAIN
                                                                                            SIGNAL
                                                                                                                                                                                                                                    EMBL; D83331; BAA11887.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core Homology with asialoglycoprotein receptors proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizuno H., Fujimoto Z., Kolzumi M., Kano H., Atoda H., "Structure of coagulation factors IX/X-binding protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS). MEDLINE-97331317; PubMed-9187649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 24-152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 220:382-387(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96184662; PubMed-8645314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Atoda H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91332000; PubMed-1831197;
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 25
102
102
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152
36
150
102
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             BY SIMILARITY.
BY SIMILARITY.
                                          PROTEIN A CHAIN.
C-TYPE LECTIN (LONG
                                                                          COAGULATION FACTOR IX/FACTOR
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in anticoagulant
OF B CHAIN).
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, a heterodimer
                                                                             X-BINDING
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SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO OTHER MEMBERS HSSP; P23807; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Alboaggregins A and B. platelets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kowalska M.A., Tan L., Holt J. Calvete J.J., Niewiarowski S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98189535; PubMed-9531050; Kowalska M.A., Tan L., Holt J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thromb.
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                                                       ANKEYLTRYIWIGLRVQNKGQPCSS-----ISYENLVDPFECFMVSRDTRLREWFKVD
                                                                                                                                                        ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGIILLSVETALEASFVDN----VLY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLTRYIWIGLRVQNKGQPC-
                                                                                                                       DCPSDWSSYEGHCYRVFNEPQNWADAEKFCTQQHKGSHLVSFQSSEEADFVVQMTRPILN
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                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemost.
                                                                                                                                                                                                                                                                                                                                                                                    30
96
123
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152 /
--LVWIGL--SNLWNQCNSQWSDGTXLDYKXWREQFEC-LVSRTTN-NEWLSMD
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                st. 79:609-613(1998).
BINDS TO PLATELET GPIB/IX RECEPTOR SYSTEM AND STIMULATES
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17213 MW;
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40.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                        WW;
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                                                                                                                                                                                                                                                                                                                                                                                                                           C-TYPE LECTIN (
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                         Score 264.5; DB 1;
Pred. No. 3.9c-21;
!3; Mismatches 34;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE C-TYPE LECTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a; Vertebrata; Euteleostomi;
Serpentes; Colubroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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Matches 51
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P81017;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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"Amino acid sequence of the alpha subunit and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Echicetin alpha subunit.
Echis carinatus (Saw-scaled viper).
Echis carinatus (Saw-scaled viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Echis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HETERODIMER OF ALPHA AND BET-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peng M., Lu W., Beviglia L., Niewiarowski S., Kirby E.P.; "Echicetin: a snake venom protein that inhibits binding of vo "illebrand factor and alboaggregins to platelet glycoprotein Blood 81:3321-328(1993).
-i- FUNCTION: BINDS TO PLATELET GPIB AND INHIBITS PLATELET AGGLUTINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the alpha and beta subunits of carinatus (saw-scaled viper)."; Biochem. J. 323:533-537(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom;
MEDLINE=97250657; PubMed=9163349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=40353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venom; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93244424; PubMed=8481512;
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119
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                                                                                                                                                                                                                                              DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYAN
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CEFKFPFVCKAKIPR
                                             CEQQHSFICKFTRPR 126
                                                                                               LPKSAIEDRVWIGLRDRSKREQCGHLWTDNSFVHYEHVVPPTKCFVLERQTEFRKWIAVN
                                                                                                                                    --KEYLTRYIWIGLRVQNKGQPC-----SSISYENLVDPFECFMVSRDTRLREWFKVD
                                                                                                                                                                                              DQDCLSGWSFYEGHCYQLFRLK-TWDEAEKYCN-QWDGGHLVSIESNAKAEFVAQLISRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P23806; 11XX
                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001304; lectin_c.
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102
81
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37.8%;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-75 IN BETA CHAIN)
SIMILARITY).
                                                                                                                                                                                                                                                                                              Score 264.5; DB 1;
Pred. No. 4.3e-21;
2; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pha subunit and computer modelling echicetin from the venom of Echis
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Best Local
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P23807; 091247;
01-NOV-1991 (Rel. 2
15-JUL-1998 (Rel. 2
15-JUL-1998 (Rel. 3
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
Alboaggregin A subunit 3.
Trimeresurus albolabris (White-lipped pit viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
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SEQUENCE
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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P81113;
                                                                                                                                      Coagulation factor (IX/X-BP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kowalska M.A., Tan L., Holt J.C., Calvete J.J., Niewiarowski S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98189535; PubMed=9531050;
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NCBI_TaxID=88087;
[1]
                                                                                                                  Trimeresurus flavoviridis (Habu).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venom;
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-!- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         platelets."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Venom
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                                                                                                                                                                                                                                                                                                                                                                                            117 RYPVCKF 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y--DEVWMGL--SDIMKECTKEWSDGARLDKKAWSGKSYC-LVSKTIN-NEWLSMDCSRT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLTRYIWIGLRVQNKGQPCSS-----ISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCPFGWSSYEGYCYKVYNKKMNWEDAESFCREQHKRSHLVSFHSSGEVDFVVSKTFPILR 62
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32
98
125
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                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79:609-613(1998).
NDS TO PLATELET GPIB/IX RECEPTOR SYSTEM AND STIMULATES
                                                                                                                                                                               20, Created)
36, Last sequence update)
36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 C
15 B
121 B
113 B
14798 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.4%;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 205.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                            146
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                                                                                                                                                            precursor
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Best Local S
Matches 43
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DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mizuno H., Fujimoto Z., Kolzumi M., Kano H., Atoda H., Morita T.;
"Structure of coagulation factors IX/X-binding protein, a heterodimer
of C-type lectin domains.";
Nat. Struct. Biol. 4:438-441(1997).
-I- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
-I- FUNCTION: ANTICOAGULANT PROTEIN WHITH A 1 TO 1 STOICHIOMETRY.
-I- SUBUNIT: HETERODIMER OF CHAINS A ND B LINKED BY A DISULFIDE BOND.
-I- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
-I- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from snake venom.";
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
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PDB; 1IXX; 06-MAY-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96184662; PubMed-8645314;
Matsuzaki R., Yoshihara E., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97331317; PubMed-9187649;
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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138
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                                                                                                                              DCPSDWSSYEGHCYKPFSEPKNWADAENFCTQQHAGGHLVSFQSSEEADFV--VKLAFQT 81
AQFVCEF 144
                                HSFICKF 122
                                                                FGHSIFWMGL--SNVWNQCNWQWSNAAMLRYKAWAE--ESYCVYFKSTNNKWRSRACRMM
                                                                                            YLTRYIWIGLRVQNKGQPC-----SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
                                                                                                                                                           ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
                                                                                                                                                                                             Similarity 33.9
43; Conservative
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                                                                                                                                                                                                                                                                             146
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98
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266:14903-14911(1991).
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36
142
98
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                                                                                                                                                                                                                                                                               16922
                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                               23;
                                                                                                                                                                                           Score 204.5; DB Pred. No. 1e-14; 3; Mismatches
                                                                                                                                                                                                                                                                                                        COAGULATION FACTOR IX/FACTOR X-BINDING PROTEIN B CHAIN.
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-102 OF A CHAIN).
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8 E1961C59F96757C CRC64;
                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                               Indels
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RESULT 12
BOTB_BOTB_B
ID BOTB_B
AC P22030
DT 01-JUL
DE BOTTOCO
OS BOTTOCO
OC Lepido
OC Lepido
OC Viperi
RN 1117
RN 1117
RN 1117
RN 11217
RN 125016
RT Prime
RT Prime
RT Prime
RT FUNCLIN
RT ISOLA
RT ISOL
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Best Local Similarity
Matches 47; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOTB_BOTJA STANDARD; PRT; 125 AA. P22030; P22030; P1-JUG-1991 (Rel. 19, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 01-JUL-1993 (Rel. 26, Last annotation update) Botrocetin, beta chain (Platelet coagglutinin).
                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venom; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca."; Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bothrops jararaca (Jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
NCBI_TaxID=8724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujimura Y., Titani K., Usami Y., Su
Fukui H., Sugimoto M., Ruggeri Z.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P23807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; C37958; C37958.
PIR; B47267; B47267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - !- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              functionally distinct forms of botrocetin, the platelet isolated from the venom of Bothrops jararaca.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91129280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93157385; PubMed-8430107;
Usami Y., Fujimura Y., Suzuki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, AND DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation and chemical characterization of two structurally and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-40.
     112
                                                        58
                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWF, AND THE COMPLEX THEN BINDS TO PLATELET GPIB, RESULTING 1 PLATELET AGGLUTINATION.

FUNCTION: THERE ARE TWO DISTINCT FORMS OF THE VON WILLEBRAND FACTOR-DEPENDENT PLATELET COAGGLUTININ. THE DIMERIC FORM IS 34-TIMES MORE ACTIVE THAN THE ONE-CHAIN BOTROCETIN IN PROMOT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: DISULFIDE-LINKED DIMER OF AN ALPHA AND A BETA CHAIN. VWF AND BOTROCETIN FORM A SOLUBLE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWF BINDING TO PLATELETS.
  CEQQHSFICKF 122
                                                          MLKGDVVWIGLSDVWNK - - -
                                                                                                                                                                                         ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE
                                                                                                       YLT-RYIWIGLR-VQNKGQPC-----SSISYEN--LVDPFECFMVSRDTRLREWFKVD 111
                                                                                                                                                                DCPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFQSKEEADFVRSL---TSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                           98
125 ∤
                                                                                                                                                                                                                                                                          Conservative
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75
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                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           113
15037 MW;
                                                                                                                                                                                                                                                                                                 29.1%;
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                                                          -CRFEWTDGMEFDYDDYYLIAEYEC-VASKPTN-NKWWIIP 112
                                                                                                                                                                                                                                                                                              Score 203.5; DB 1;
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (WITH C-80 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                              1ED2027ED817FCA0 CRC64;
                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ozeki Y., Nishio K., Fukui H.,
                                                                                                                                                                                                                                                                          39;
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                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                          Length 125;
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RESULTING IN
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ECHBERT RESULT REPRESENTATION OF COCCEPT REP
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                                                                                                                              Query Match
Best Local S
Matches 39
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P81996;
30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                      DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Echis carinatus (Saw-scaled viper).
Echis carinatus (Saw-scaled viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                         DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polgar J., Magnenat Clemetson K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECHCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peng M., Lu W., Beviglia L., Niewiarowski S., Kirby E.P.; "Echicetin: a snake venom protein that inhibits binding of vowillebrand factor and alboaggregins to platelet glycoprotein Blood 81:2321-2388(1993).

-I- FUNCTION: BINDS TO PLATELET GPIB AND INHIBITS PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Amino acid sequence of the alpha subunit and the alpha and beta subunits of echicetin from carinatus (saw-scaled viper) ";
Biochem. J. 323:533-537(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95091801; P
Peng M., Holt J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lepidosauria; Squamata; Scl. Viperidae; Viperinae; Echis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Echicetin beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: HETERODIMER OF ALPHA
-!- SIMILARITY: CONTAINS 1 C-TYPE
HSSP; P23807; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97250657; PubMed=9163349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation, characterization and amino acid sequence of subunit, a specific inhibitor of von Willebrand factor a interaction with glycoprotein Ib.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=40353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93244424; PubMed=8481512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                            NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
                                                                                                                                                                                                                                                                                                                                                                                                 enom;
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64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGLUTINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : :|:|:|
CTRFKNFVCEF
                                                                        CPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKEY
  LTRY IWIGLRVQNKGQPC----
                                            CLPDWSVYEGYCYKVFKERMNWADAEKFCMKQVKDGHLVSFRNSKEVDFMISLAFPMLK-
                                                                                                                                                                                                                                                                                            PS50L

PS50L

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                                                                                                                                                                                                                                         96
123 i
                                                                                                                                Conservative
                                                                                                                                                                                                                                           AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
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39,
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13
119
75
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                                                                                                                                                     27.48;
31.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence
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                                                                                                                                                                                                                                           MW;
                                                                                                                                24;
  ---SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
                                                                                                                              Score 191.5;
Pred. No. 2e-1
24; Mismatches
                                                                                                                                                                                                                                                            C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                           C42COAD7CDE18CA6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND BETA SUBUNITS
                                                                                                                                                   191.5; DB
No. 2e-13;
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                                                                                                                                                                          DВ
                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            computer modelling
the venom of Echis
                                                                                                                                                                     1;
                                                                                                                                Indels
                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saqi M.S.A.,
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                                                                                                                                13;
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                                                                                                                                Gaps
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LITA_HUMAN
ID LITA_H
AC P05451
DT 01-NOV
DT 01-OCT
DT 16-OCT
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Best Local :
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01-NOV-1988
01-OCT-1989
16-OCT-2001
                                                                  LITA_HUMAN
P05451; P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
SEQUENCE
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p81116;
p15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
115-JUL-1998 (Rel. 36, Last sequence update)
115-JUL-
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SMART: SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P23807; 1IXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS, DISULFIDE-LINKED -i- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Alboaggregins A and B. Structure and interaction with human platelets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kowalska M.A., Tan L., Holt J. Calvete J.J., Niewiarowski S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98189535; PubMed=9531050; Kowalska M.A., Tan L., Holt J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venom;
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Gross J., Carlson Wands J.R.;
"Isolation, chara pancreatic human
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J. Biol. Chem.
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J. Biol.
[2]
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de Caro A.M.;
"Partial amino acid sequence of human
novel pancreatic secretory protein.";
Biochem. J. 238:227-232(1986).
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                                                                                                                                                                                                 pancreatic stone protein. The 5-oxoproline glycosylated on the 5th amino acid residue. Blochim. Blophys. Acta 994:281-284(1989).
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"N-terminal sequence extension in the glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86086356;
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Dagorn J.-C
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"Complete nucleotide sequence of human reg gene and its expression normal and tumoral tissues. The reg protein, pancreatic stone protein, and pancreatic thread protein are one and the same product
Rouimi P., Bonicel J., Rovery M., de "Cleavage of the Arg-Ile bond in the human pancreatic stone protein.";
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89150292; PubMed-2493268;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 23-47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87099950; PubMed-3541906; Montalto G., Bonicel J.J., Multigner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 34-98.
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"Complete amino acid sequence of an
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MEDLINE-88029417; PubMed-3665916;
MEDLINE-88029417; PubMed-3665916;
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                                                                                                    SEQUENCE OF 33-58.
MEDLINE~87219142;
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Mammalia; Eutheria;
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Chem. 263:2111-2114(1988).
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Metazoa; Chordata; Chord
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                                                                                                       PubMed=3108036;
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                                   Caro A.;
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ne N-terminal chain
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pancreatitis.";
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AAA60546.1; AAA60545.1; AAA36558.1; AAA36559.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerbaud V., Pignol D., Loret E., Bertrand J.A., Berland Fontecilla-Camps J.C., Canselier J.P., Gabas N., Verdier "Mechanism of calcite crystal growth inhibition by the Nundecapeptide of lithostathine.";
Biol. Chem. 275:1057-1064(2000).
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Protein Eng. 9:949-957(1996)
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de Reggi M.
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MEDLINE=96256285; PubMed=8654365;
Bertrand J.A., Pignol D., Bernard J.-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        three-dimensional structure modeling
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MEDLINE=97120677; PubMed=89
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"Crystal structure of human lithostathine, of stone formation.";
DMBO J. 15:2678-2684(1996).
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Itoh T., Tsuzuki H.,
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                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: HIGH EXPRESSION LEVELS IN FETAL AND I BRAINS; MUCH LOWER IN ADULT BRAINS.
DISEASE: ALZHEIMER'S DISEASE AND DOWN'S SYNDROME PATIENTS ENHANCED EXPRESSION OF PSP-RELATED TRANSCRIPTS AND INTRANSACCUMULATION OF PSP-LIKE PROTEINS IN THEIR BRAINS.
SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                            FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION. MAY BE ASSOCIATED WITH NEURONAL SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION TISSUE SPECIFICITY: IN PANCREATIC ACINAR CELLS AND, IN LOWER LEVELS, IN BRAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       function for human lithostathine?:
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i., Katoh T., Teraoka
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Search completed: October 3, 2002, 16:29:02 Job time: 231 sec
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InterPro; IPR003990; pancreatitis_assoc.
Pfam; PF00059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMARR; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Glycoprotein; Signal; Alzheimer's disease; Down's syndrome; Lectin; 3D-structure.
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150 KDVPCEDKFSFVCKF 164
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; IQDD; 24-JAN-00.
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LITHOSTATHINE 1 ALPHA.
166
C-TYPE LECTIN (LONG FORM).
23
PYRROLIDONE CARBOXYLIC ACID.
27
O-LINKED.
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SSY -> NSF (IN REF. 3).
7
C -> S (IN REF. 3).
13
C -> L (IN REF. 3).
10
G -> A (IN REF. 2).
18731 MW; EF93C760DC2DBCC3 CRC64;
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C-TYPE LECTIN (LONG FORM).
PYRROLIDONE CARBOXYLIC ACID.
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| mus lydra gall gaenc lach | 7777 | O62623 bos taurus Q9nt67 homo sapien Q9hbk4 homo sapien Q96gw7 homo sapien Q96fp7 homo sapien Q96fp7 homo sapien Q90wm2 xenopus lae | Q9deal agkistrodon Q9psm5 bothrops ja Q25459 megabalanus Q9byz8 homo sapien Q9qyf7 mesocricetu Q9ps19 trimeresuru | Q9dg31 agkistrodon Q9psm8 echis carin Q98sm5 agkistrodon Q9def8 agkistrodon Q9yqn4 agkistrodon |

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Q9DEA2;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AGKICETIN ALPHA SUBUNIT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen Y.L., Hong T.M., Chang T., Tsai I.H.; "CDNA sequence and functional characterization of glycoprotein binding protein from the venom of Deinagkistrodon acutus."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF102901; AAG42040.1; -.

HSSP; P23806; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00059; lectin_c; 1. SMART; SM00034; CLECT; 1.
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Score 383; Db +-, pred. No. 4.7e-35;
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AGKICETIN ALPHA SUBUNIT.
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agkistrodon

Qy

ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE

Query Match
Best Local Similarity
Matches 72; Conserv

Conservative

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Length 155; Indels

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Gaps

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O9YGG9;
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
Signal
SEQUENCE
                                                 OPPSM6 PRELIMINARY; PRT; 142 AA.

OPPSM6; PART 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

PLATELET GLYCOPROTEIN IB-BINDING PROTEIN ALPHA SUBUNIT,

SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-98319530; PubMed-9657448;

MEDLINE-98319530; PubMed-9657448;

Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasa
Suzuki M., Matsui T., Titani K., Yoshioka A.;

"The CNA cloning and molecular characterization of a
platelet glycoprotein Ib-binding protein, mamushigin,
halys bromhoffii venom.";
Thromb. Haemost. 79:1199-1207(1998).

EMBL; AB019615; BAA34424.1; -.

HSSP; P23806; IIXX.
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01-MAY-1999 (TrEMBLrel. 11, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAMUSHIGIN ALPHA PRECURSOR.
Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Lepidosaurla; Squamata; Scleroglossa; Serpentes; Colubroidea
Viperidae; Crotalinae; Agkistrodon.
Bothrops jararaca
Eukaryota; Metazoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT;
PROSSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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                                                                                                                                                                                                                                                                                                                                                   CGQKYAFMCKFLRPR 157
                                                                                                                                                                                                                                                                                                                                                                                 CEQQHSFICKFTRPR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYAN
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:| |:||: :||
LKHVFMCKYLKPR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSDCPSDWSSNGRFCYKLFQQKMKWADAERFCTEQRTGAHLVSIESNTEAAFVNQMISEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IK-KTDYVWIGLTVQNEEQQCKSRWSDRSSVSYENLVKPNSKKCFVLKEYEGSRKWFNVY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - IKPYVWIGLRVQNEGQQCSSKWSDSSKVSYENLVEPFSKKCFVLKKDTGFRTWENVYCG
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                           (Jararaca)
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18333 MW;
     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.2%;
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Pred. No. 3e-32;
5; Mismatches
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47DAA17891CE1865 CRC64;
Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157
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Serpentes; Colubroidea;
  Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 157;
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     Euteleostomi;
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from Agkist
                                                                                  GPIB-BP
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Best Local
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                         Q98UJ0
Q98UJ0;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                           Tani A., Ogawa T., Nose T., Nikandorov N.N., Deshimaru N.Chang C., Fukumaki Y., Ohno M.;
"Characterization and molecular evolution of an anticoac from Agkistrodon actus venom.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046491; BAB21452.1; -.
HSSP; P23806; 11XX.
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pfam; pF00059; lectin_c; 1.
smarr; sM00034; CLECT; 1.
pROSITE; pS00615; C_TYPE_LECTIN_1;
pROSITE; pS50041; C_TYPE_LECTIN_2;
SEQUENCE 142 AA; 16720 MW; E28E
                                     PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

SEQUENCE 146 AA; 16461 MW; 6ADF0E032544316C
                                                                                                     InterPro; IPR001304; lectin_c.
InterPro; IPR003990; pancreatitis_assoc
Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                      Trimeresurus flavoviridis (Habu)
Eukaryota; Metazoa; Chordata; Cr
                                                                                                                                                                                                                                                                                            Lepidosauria; Squamata;
Viperidae; Crotalinae; 1
                                                                                                                                                                                                                                                                                                                                                              FACTOR XI/FACTOR X BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viperidae; Crotalinae; Bothrops.
NCBI_TaxID=8724;
                                                                             PRINTS; PR01504; PNCREATITSAP SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=VENOME GLAND;
                                                                                                                                                                                                                                                                               NCBI_TaxID=88087;
                                                                                                                                                                                                                                                                                                                                                   XI/XBP-A.
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HSSP; P23806; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 KVDCEQQHSFICKFTRPR 126
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47.18;
45
                                                                                                                                                                                                                                                                                              ; Scleroglossa; Trimeresurus.
.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
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Last annotation update)
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Pred.
Score
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                                                                                                                                                                                                                                                                                                                        Craniata;
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314.5;
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                                                                                                                                                                                                                                                                                                                                                              CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                                                                                                                                                         Serpentes;
                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi; erpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
..6e-30;
nes 34;
 DВ
                                                                                                                                                                                                                             Deshimaru M.,
 13;
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                                        CRC64;
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Best Local S
Matches 58
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                                093426 PRELIMINARY;
093426;
01-NOV-1998 (TrEMBLrel. 08, C
01-NOV-1998 (TrEMBLrel. 17, L
01-JUN-2001 (TrEMBLrel. 17, L
CONVULXIN ALPHA PRECURSOR.
CVX ALPHA.
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(9YGN5;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FIBRINOGEN CLOTTING INHIBITOR A CHAIN.
Agkistrodon halys brevicaudus (Korean slamosa snake)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001304; lectin_c.
pfam; pF00059; lectin_c; 1.
sMART; SM00034; CLECT; 1.
proSITE; pS00615; C_TYPE_LECTIN_1; 1.
proSITE; pS50041; C_TYPE_LECTIN_2; 1.
sEQUENCE 154 AA; 17293 MW; 8D06F7DDFA0D140D CRC64;
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Kim D.S., Koh Y.S.;

"Purification and molecular cloning of snake venom fibrin clotting inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF125309; AAD18055.1; -. HSSP; P23806; 1IXX.
   Crotalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viperidae; Crotalinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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Pred. No. 2.1
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TISSUE=VENOM GLAND;
Ogawa T., Tani A.;
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Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon. Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning of subunits of convulxin, a collagen-like platelet-aggregating protein from Crotalus durissus terrificus venom.";
Biochem. J. 33:389-393(1998).
-i- EUNCTION: BINDS TO THE PLATELET AND COLLAGEN RECEPTOR,
GLYCOPROTEIN VI (GPVI).
-i- SUBUNIT: HETEROHEXAMER OF THREE ALPHA CHAINS AND THREE BETA
                                                                                                                                                                                        ANTICOAGULANT PROTEIN A PRECURSOR.
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SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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SEQUENCE FROM N.A.
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| EESFSHVSIGLRVQNKEKQCSTKWSDGSSVSYDNLLDLYITKCSLLKKETGFRKWFVASC
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C-TYPE LECTIN (LONG E
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 2.2e-26;
B; Mismatches 36;
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BY SIMILARITY.
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949F9C6D673E2318 CRC64;
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Best Local S
Matches 56
                                                                                                                           Query Match
Best Local (
                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SOON Y.D., Kim D.S., Jang Y.S., Chung K.H.;

KOO B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;

A novel coagulation factor Xa inhibitor from Korean sna

(Agkistrodon halys) venom.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF190827; AAG17178.1;

INTERPO; IPR001304; lectin_c.

Interpo; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                         Signal.
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                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                        Pfam; PF00059; lectin_c; 1.
SMART; SMO0034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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Viperidae; Crotalinae; Gloydius.
NCBI_TaxID-8714;
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pfam; pF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
pROSITE; pS00615; C_TYPE_LECTIN_1; 1.
pROSITE; pS50041; C_TYPE_LECTIN_2; 1.
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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QQHSFICK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRDPFVCE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAKIHVWIGLRAQNKEKOCSIEWSDGSSISYENWIEEESKKCLGVHKATGFRKWENFYCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCSSSWSSYEGHCYKAFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIK
                                                                                                                           Similarity
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24
152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                         23 F
152 F
17455 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 F
17124 MW;
                                                                                                                        43.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                 Score 300.5;
Pred. No. 7.6e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 300.5; DB 1
Pred. No. 7.6e-26;
5; Mismatches 38
                                                                                                                                                                                                                         HALYXIN A-CHAIN.
BDD74D1DC280C28D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. ; 5C59C0F503A4D223 CRC64;
                                                                                                                                                                                                                                                                                                                             ٠.
                                                                                              1.6e-26;
hes 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chung K.H.; from Korean snake
                                                                                                                                                DB 13; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                              Gaps
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RESULT 10
Q9IAMO
ID Q9IAMO
AC Q9IAMO
DT 01-OCT
DT 01-DEC
DT 01-DEC
DE AGKISA
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Q91841
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Best Local :
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O9IAMO;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
AGKISACUTACIN B CHAIN.
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SEQUENCE
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Q91841;
Q91841;
Q1-QT-2000 (TrEMBLrel. 15, Created)
Q1-QT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AGGRETIN ALPHA CHAIN (FRAGMENT).
AGKISTROGOR THOGOSTOMA (Malayan pit viper) (Calloselasma rhodostoma).
AGKISTYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Calloselasma.
NCBI_TaxID=8717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-VENOM GLAND;

MEDLIND-99443731; PubMed-10512747;

Chung C.H., Au L.C., Huang T.F.;

"Molecular cloning and sequence analysis of aggretin,
platelet aggregation inducer.";

Bliochem. Biophys. Res. Commun. 263:723-727(1999).
                                                                                                                                                   Q9IAM0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chung C.H., Au L.C., Huang T.F.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF244900; AAF79952.1;
HSSP; P23806; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                             112 CEQQHSFICK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 YLT--RYIWIGLRVQNKGQPC-----SSISYENLVD--PFECFMVSRDTRLREWFKVD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                      63 ELADEDYVWIGLRAQNKEQQCSSEWSDGSSVSYENLIDLHTKKCGALEKLTGFRKWVNYY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AA;
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                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                           132
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15796 MW; 3B474A4149F0027A CRC64;
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43.8%;
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                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 296; DB 13;
Pred. No. 2.1c-25;
3; Mismatches 38;
                                                                                                                                                   146
                                                                                                                                                   A
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Best Local
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                                                                                                                                                                                                                                                                                                                                           093427 PRELIMINARY;
093427;
01-NOV-1998 (TremBLrel. 08, C
01-NOV-1998 (TremBLrel. 08, L
01-JUN-2001 (TremBLrel. 17, L
CONVULXIN BETA PRECURSOR.
                                                                                                                                                                                                                                                   Crotalus durissus terrificus (South American rattlesnake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
NCBI_TaxID-8732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 146 AA; 16726 MW; 7360B6D6864131BB CRC64;
                                                                                                        Leduc M., Bon C.:

"Cloning of subunits of convulxin, a collagen-like platelet-
"Cloning protein from Crotalus durissus terrificus venom.

Biochem. J. 333:389-393(1998).

-!- FUNCTION: BINDS TO THE PLATELET AND COLLAGEN RECEPTOR,

GLYCOPROTEIN VI (GPVI).

-!- SUBUNIT: HETEROHEXAMER OF THREE ALPHA CHAINS AND THREE B
             Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                     -!- SIMILARITY: TO OTHER MEMBERS EMBL; Y16349; CAA76182.1; -. HSSP; P23807; 1IXX.
                                                                                                                                                                                                       TISSUE=VENOM GLAND;
MEDLINE=98324901; P
                                                                                                                                                                                                                                                                                                                                     CVX BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agkistrodon acutus venom.";
Submitted (AUG-1999) to the
EMBL; AF176421; AAF26287.1;
HSSP; P23807; 1IXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheng X., Qian Y.,
Liu J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agkistrodon acutus (Hundred pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=36307;
 PROSITE;
                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Agkisacutacin, a new fibrinolytic & anti-platelet protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVCKF 144
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 PS00615;
                                       IPR001304; lectin_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
 C_TYPE_LECTIN_1; 1.
                                                                                                                                                                                                            PubMed=9657980;
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43.2%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Pred. No. 1.7e-21;
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                                                                                  QF
                                                                                 THE C-TYPE LECTIN FAMILY
                                                                                                                                                                                                                                     24-53;
                                                                                                                                                                                                                                                                                                                                                                                                                      148
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                                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                                           AND THREE BETA
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Дb
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Best Local (
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Best Local Similarity
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Q9IAM1;
Q9IAM1;
C9IAM1;
O1-CCT-2000 (TrEMBLrel. 15, L)
O1-CCT-2000 (TrEMBLrel. 15, L)
O1-DEC-2001 (TrEMBLrel. 19, L)
AGKISACUTACIN A CHAIM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Sculamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                     Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; LECTIN_2; 1.
PROSSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 135 AA; 15041 MW; F9A55A3802AFA291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Agkistrodon acutus venom.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF176420; AAF26286.1; -
HSSP; P23806; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=36307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Agkisacutacin, a new fibrinolytic &
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 SFVCKF
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  84
                                          63
                                                                                       24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LTRYIWIGLRVQNKGQPC-----SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
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SAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIE
                                        YLTRYIWIGLRVQNKGQPC-----SSISYENLVD
                                                                                                            ECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPSHWSSYDRYCYKVFKQEMTWADAEKFCTQQHTGSHLVSFHSTEEVDFV--VKMTHQSL
                                                                                  CSSGWSSYEGHCYKVFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X., Qian Y., Liu Q., Li B.X.Y., Ding J.,
                                                                                                                                                                           l Similarity
47; Conserv
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148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                                                                                           19;
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Last sequence update)
Last annotation updat
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                         Score 260.5; DB 13;
Pred. No. 1.9e-21;
9; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 261.5; D. Pred. No. 1.7e-
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BY SIMILARITY.
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RESULT
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1DPSM9
1DPSM9
AC Q9E
DT Q1
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RESULT OF THE RE
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Best Local
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Q9PSM9;

Q1-MAY-2000 (TrEMBLrel. 13, Created)

Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Q1-MAY-2000 (TrEMBLrel. 17, Last annotation update)

Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)

ECLY IX/X-BP ALPHA SUBUNIT=COAGULATION FACTOR IX/FACTOR X-BINDING PROTEIN ALPHA SUBUNIT

ECH1s carinatus (Saw-scaled viper).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperinae; Echis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91840 PRELIMINARY; PRT; 146 AA.
Q91840;
Q10-Q1840;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AGGRETIN BETA CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 35:5264-5271(1996).
HSSP; P23806; IIXX.
Interpro; IPR001304; lectin_c.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
PROSITE; PS00611; C_TYPE_LECTIN_2; 1.
SEQUENCE 131 AA; 15439 MW; B85E6C5CBF317E
                                                                                  chung C.H., Au L.C., Huang T.F.;
"Molecular cloning and sequence analysis of aggretin, platelet aggregation inducer.";
Biochem. Biophys. Res. Commun. 263:723-727(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Calloselasma.
NCBI_TaxID=8717;
SEQUENCE
                                                                                                                                                                                                                                                                    TISSUE-VENOM GLAND;
MEDLINE-99443731; PubMed-10512747;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen Y.L., Tsai I.H.;
"Functional and sequence characterization of coagulation factor "Functional and sequence characterization of Echis carinatus "Liviactor X-binding protein from the venom of Echis carinatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96196635; PubMed-8611513; Chen Y.L., Tsai I.H.;
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45; Conser
FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B85E6C5CBF317E24 CRC64;
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Best Local S
Matches 50
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon. NCBI_TaxID=36307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q90WL9 PRELIMINARY; PRT; 124 AA.
Q90WL9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
AKITONIN (FRACMENT).
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Chung C.H., Au L.C., Huang T
Submitted (MAR-2000) to the
EMBL; AF244901; AAF79953.1;
HSSP; P23807; LIXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001304; lectin_c. Pfam; PF00059; lectin_c; 1. SMART; SM0034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Zha X.D., Xu K.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 CSFVCKF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 HSFICKF 122
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                                                                                                                                                                                                                                                        2 LECPSGWSSYDRYCYKPFKQEMTWADAQRFCSEQAKGGHLLSVETALEASFVDNVLYANK 61 ::||| |||| :| :| | || : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
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SFVCEF
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                                                                                                                                               EYLTRYIWIGLR-VQN----KGQPCSSISYENLVDPFKCFMVSRDTRLREWFKVDCEQQH 116
                                                                                                                                                                                                                        MDCPSDWSSYEGNCYLVVKEKKTWAEAQKFCTEQRKECHLVSFHSAEEVDFVVSKTFPIL 60
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                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16770 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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Pred. No. 7.9e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                 Score 229.5; DB 13; Length 124; Pred. No. 5.1e-18; Pred. No. 43; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930839140CFD8908 CRC64,
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